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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/047,264A

DATE: 07/16/2002 P.6
TIME: 16:41:16

Input Set : A:\Gi-532.app

Output Set: N:\CRF3\07162002\J047264A.raw

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3 <110> APPLICANT: Fouser, Lynette
4     Liu, Wei
5     Deng, Bijia
7 <120> TITLE OF INVENTION: TYPE 2 CYTOKINE RECEPTOR AND NUCLEIC ACIDS ENCODING
8     SAME
10 <130> FILE REFERENCE: 22058-532
12 <140> CURRENT APPLICATION NUMBER: 10/047264A
13 <141> CURRENT FILING DATE: 2002-01-14
15 <150> PRIOR APPLICATION NUMBER: 60/261442
16 <151> PRIOR FILING DATE: 2001-01-12
18 <150> PRIOR APPLICATION NUMBER: 60/267021
19 <151> PRIOR FILING DATE: 2001-02-06
21 <150> PRIOR APPLICATION NUMBER: 60/270835
22 <151> PRIOR FILING DATE: 2001-02-23
24 <160> NUMBER OF SEQ ID NOS: 39
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30 <212> TYPE: DNA
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36 tttcacaaca ttttgcaatg gcagcctggg agggcactta ctggcaacag cagtgtctat 180
37 tttgtgcagt acaaaatata tggacagaga caatggaaaa ataaagaaga ctggtgggg 240
38 actcaagaac tctctgtga ccttaccagt gaaacctcag acatacagga acctattac 300
39 gggaggggtg gggcgccctc ggctgggagc tactcagaat ggagcatgac gccgcgggttc 360
40 actccctggg gggaaacaaa aatagatcct ccagtcatga atataaccca agtcaatggc 420
41 tctttgttgg taattctcca tgctccaaat ttaccatata gataccaaaa ggaaaaaaat 480
42 gtatctatag aagattacta tgaactacta taccgagttt ttataattaa caattcacta 540
43 gaaaaggagc aaaagggtta tgaaggggct cacagagcgg ttgaaattga agctctaaca 600
44 ccacactcca gctactgtgt agtggctgaa atatatcagc ccatgttaga cagaagaagt 660
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49 <211> LENGTH: 231
50 <212> TYPE: PRT
51 <213> ORGANISM: human
53 <400> SEQUENCE: 2
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55 1 5 10 15
57 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
58 20 25 30
60 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln

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61          35          40          45
63 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
64          50          55          60
66 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
67 65          70          75          80
69 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
70          85          90          95
72 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
73          100          105          110
75 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
76          115          120          125
78 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
79          130          135          140
81 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
82 145          150          155          160
84 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
85          165          170          175
87 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
88          180          185          190
90 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
91          195          200          205
93 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
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96 Glu Arg Cys Val Glu Ile Pro
97 225          230
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101 <211> LENGTH: 792
102 <212> TYPE: DNA
103 <213> ORGANISM: human
105 <400> SEQUENCE: 3
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107 ggaactcagt caacgcatga gtctctgaag cctcagaggg tacaatttca gtcccgaat 120
108 tttcacaaca ttttgcaatg gcagcctggg agggcactta ctggcaacag cagtgtctat 180
109 tttgtgcagt acaaaatcat gttctcatgc agcatgaaaa gctctcacca gaagccaagt 240
110 ggatgctggc agcacatttc ttgtaacttc ccaggctgca gaacattggc taaatatgga 300
111 cagagacaat ggaaaaataa agaagactgt tggggctactc aagaactctc ttgtgacctt 360
112 accagtgaat cctcagacat acaggaacct tattacggga ggggtgagggc ggcctcggct 420
113 gggagctact cagaatggag catgacgccg cggttcactc cctgggtggga aacaaaaata 480
114 gatcctccag tcatgaatat aacccaagtc aatggctctt tgttggtaat tctccatgct 540
115 ccaaatttac catatagata ccaaaggaa aaaaatgtat ctatagaaga ttactatgaa 600
116 ctactatacc gagtttttat aattaacaat tctactagaa aggagcaaaa ggtttatgaa 660
117 ggggctcaca gagcggttga aattgaagct ctaacaccac actccagcta ctgtgtagt 720
118 gctgaaatat atcagcccat gtttagacaga agaagtcaga gaagtgaaga gagatgtgtg 780
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123 <211> LENGTH: 263
124 <212> TYPE: PRT
125 <213> ORGANISM: human
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Input Set : A:\Gi-532.app

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128 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
129   1           5           10           15
131 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
132           20           25           30
134 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
135           35           40           45
137 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
138           50           55           60
140 Lys Ile Met Phe Ser Cys Ser Met Lys Ser Ser His Gln Lys Pro Ser
141   65           70           75           80
143 Gly Cys Trp Gln His Ile Ser Cys Asn Phe Pro Gly Cys Arg Thr Leu
144           85           90           95
146 Ala Lys Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
147           100          105          110
149 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
150           115          120          125
152 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
153           130          135          140
155 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
156 145           150          155          160
158 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
159           165          170          175
161 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
162           180          185          190
164 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165           195          200          205
167 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
168           210          215          220
170 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
171 225           230          235          240
173 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
174           245          250          255
176 Glu Arg Cys Val Glu Ile Pro
177           260
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181 <211> LENGTH: 393
182 <212> TYPE: DNA
183 <213> ORGANISM: human
185 <400> SEQUENCE: 5
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187 ggaactcagt caacgcatga gtctctgaag cctcagaggg tacaatttca gtcccgaat 120
188 ttccacaaca ttttgcaatg gcagcctggg agggcactta ctggcaacag cagtgtctat 180
189 tttgtgcagt acaaaatata tggacagaga caatggaaaa ataaagaaga ctgttgggg 240
190 actcaagaac tctcttgtga ccttaccagt gaaacctcag acatacagga accttattac 300
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192 actccctggt gggaaaagagc aaaaggttta tga
195 <210> SEQ ID NO: 6
196 <211> LENGTH: 130
197 <212> TYPE: PRT

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198 <213> ORGANISM: human
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201 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
202   1           5           10           15
204 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
205           20           25           30
207 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
208           35           40           45
210 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
211           50           55           60
213 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
214   65           70           75           80
216 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
217           85           90           95
219 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
220           100          105          110
222 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Arg Ala Lys
223           115          120          125
225 Gly Leu
226           130
229 <210> SEQ ID NO: 7
230 <211> LENGTH: 29
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
237 <400> SEQUENCE: 7
238 tcatggaatt tccacacatc tctcttcac
241 <210> SEQ ID NO: 8
242 <211> LENGTH: 341
243 <212> TYPE: PRT
244 <213> ORGANISM: human
246 <400> SEQUENCE: 8
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248   1           5           10           15
250 Val Ser Gly Ile Val Pro Lys Pro Arg Asn Ala Arg Ile Ser Ser Val
251           20           25           30
253 Asn Phe Arg Ser Val Leu Leu Trp Asp Pro Pro Gly Val Arg Lys Gly
254           35           40           45
256 Asn Leu Ser Tyr Thr Val Gln Ala Lys Ser Ile Phe Pro Lys Gln Asn
257           50           55           60
259 Phe Asn Asn Val Thr Thr Asn Leu Asn Val Thr Glu Cys Asp Val Ser
260   65           70           75           80
262 Ser Leu Ser Val Tyr Gly Ala Tyr Val Leu Arg Val Arg Thr Glu Trp
263           85           90           95
265 Glu Asp Glu His Ser Asp Trp Ala Val Val Arg Phe Lys Pro Met Ala
266           100          105          110
268 Asp Thr Val Ile Gly Pro Pro Ser Val Asn Val Lys Ser Glu Ser Gly
269           115          120          125

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271 Thr Leu His Val Asp Phe Thr Gly Pro Ala Ala Asp Arg Glu His Asp
272      130                      135                      140
274 Lys Trp Ser Leu Lys Gln Tyr Tyr Gly Ser Trp Ile Tyr Arg Ile Leu
275 145                      150                      155                      160
277 Tyr Trp Lys Lys Gly Ser Asn Lys Lys Val Ile His Ile Asp Thr Lys
278                      165                      170                      175
280 His Asn Ser Glu Ile Leu Ser Gln Leu Glu Pro Trp Thr Ile Tyr Cys
281                      180                      185                      190
283 Ile Gln Val Gln Gly Val Ile Pro Glu Trp Asn Lys Thr Gly Glu Arg
284                      195                      200                      205
286 Ser Gln Glu Leu Cys Glu Gln Thr Thr His Asn Gly Val Thr Pro Val
287      210                      215                      220
289 Trp Ile Val Val Thr Val Leu Leu Gly Ser Met Leu Ala Val Ile Ile
290 225                      230                      235                      240
292 Ser Val Pro Val Cys Phe Phe Ala Phe Trp Tyr Leu Tyr Arg Phe Thr
293                      245                      250                      255
295 Lys His Val Phe Phe Pro Ser Tyr Ile Phe Pro Gln His Leu Lys Glu
296                      260                      265                      270
298 Phe Phe Ser Pro Val Pro Gln Glu Glu His His Phe His Asp Trp Leu
299                      275                      280                      285
301 Thr Val Ile Ser Glu Glu Pro Lys Ser Gln Arg Asp Glu Thr Val Glu
302      290                      295                      300
304 Glu Ala Ser Arg Thr Ala Glu His His Gln Asp Ser Lys Gln Glu Ile
305 305                      310                      315                      320
307 Ser Asp Ser Glu Ile Leu Pro Pro Leu Glu Arg Asp Gln Thr Leu Leu
308                      325                      330                      335
310 Thr Leu Gln Ser Gly
311      340
314 <210> SEQ ID NO: 9
315 <211> LENGTH: 26
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
322 <400> SEQUENCE: 9
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326 <210> SEQ ID NO: 10
327 <211> LENGTH: 29
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR Primer
334 <400> SEQUENCE: 10
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339 <211> LENGTH: 728
340 <212> TYPE: DNA
341 <213> ORGANISM: human
343 <400> SEQUENCE: 11

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/047,264A

DATE: 07/16/2002
TIME: 16:41:18

Input Set : A:\Gi-532.app
Output Set: N:\CRF3\07162002\J047264A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; Xaa Pos. 7,10
Seq#:14; Xaa Pos. 11,14
Seq#:15; Xaa Pos. 2,9,13
Seq#:16; Xaa Pos. 12
Seq#:17; Xaa Pos. 2,7,18
Seq#:18; Xaa Pos. 7,9,20
Seq#:19; Xaa Pos. 5,8,13
Seq#:33; Xaa Pos. 139

VERIFICATION SUMMARY

DATE: 07/16/2002

PATENT APPLICATION: US/10/047,264A

TIME: 16:41:18

Input Set : A:\Gi-532.app

Output Set: N:\CRF3\07162002\J047264A.raw

L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:16
L:540 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:16
L:568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:1204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:128